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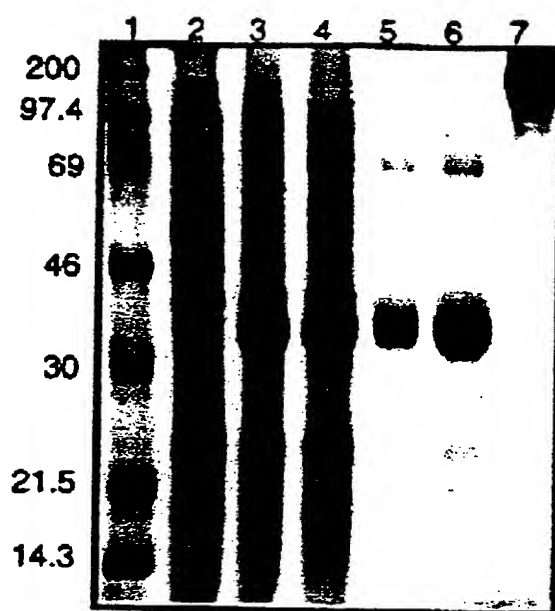
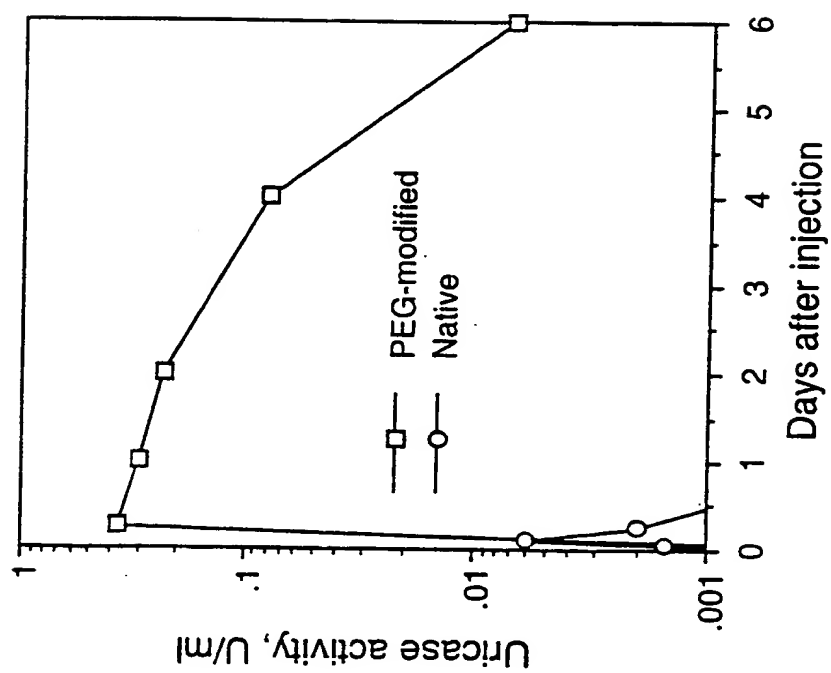
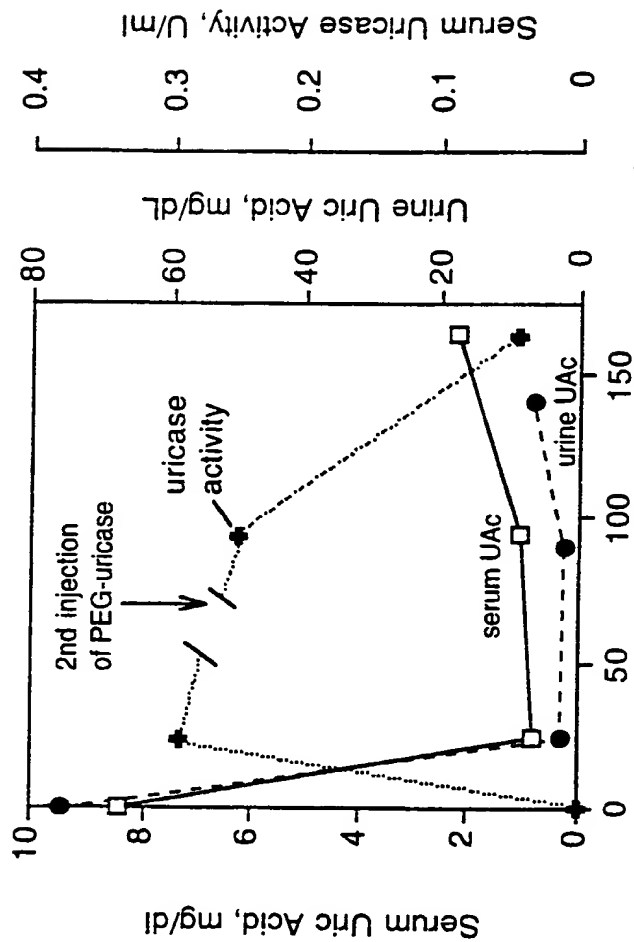


Fig. 1

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**Fig. 2**

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Hours after first injection of PEG-PBC Uricase

Fig. 3

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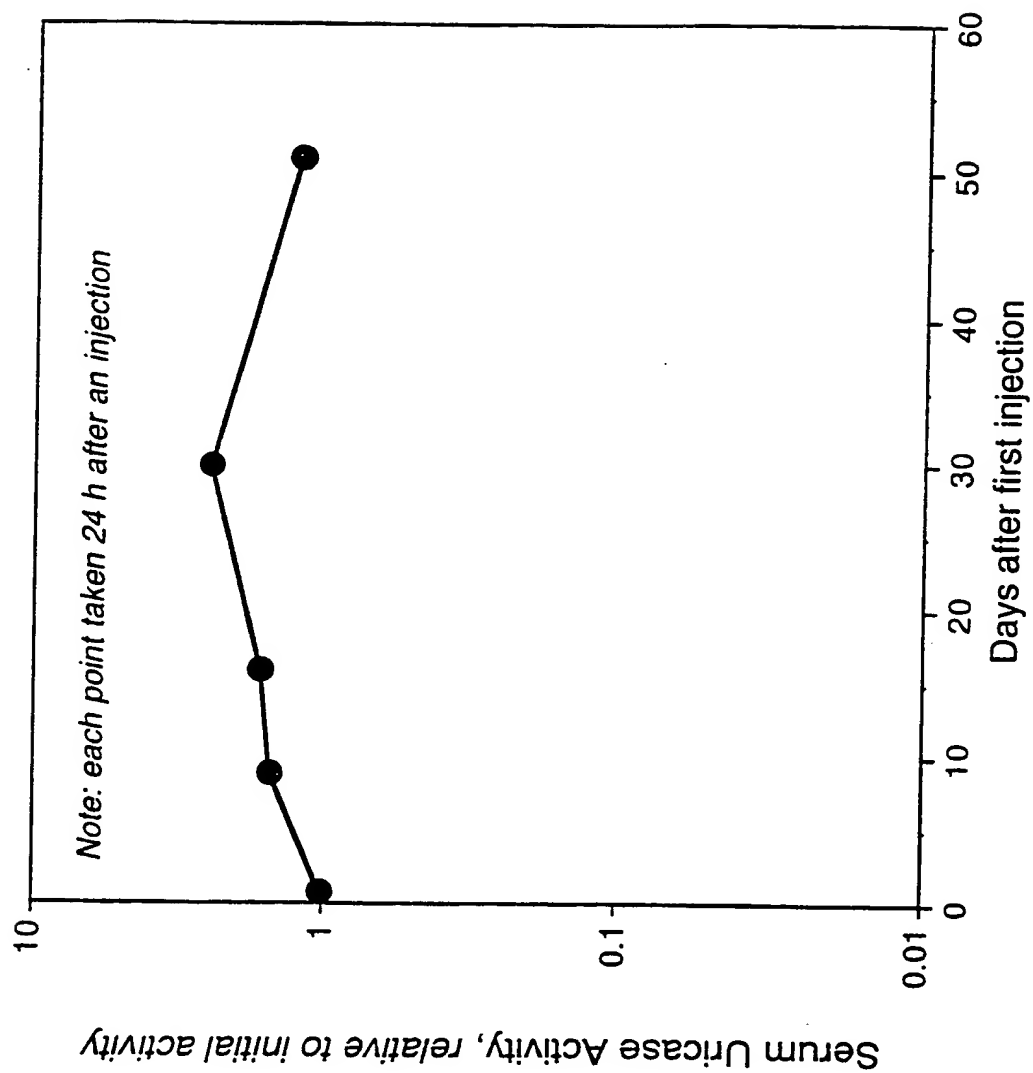


Fig. 4

Fig. 5

Deduced Amino Acid Sequences of Pig-Baboon Chimeric Uricase (PBC Uricase)

and Porcine Uricase Containing the Mutations R291K and T301S (PKS Uricase),

Compared with the Porcine and Baboon Sequences

Porcine	MAHYRNDYKK	NDEVEFVRTG	YGKDMIKVLH	IQRDGKYHSI	40
PBC	1-225 porcine sequence →				
PKS	1-288 porcine sequence →				
Baboon	MADYHNNYKK	NDELEFVRTG	YGKDMVKVLH	IQRDGKYHSI	40
Porcine	KEVATSVQLT	LSSKKDYLHG	DNSDVIPTDT	IKNTVNVLAK	80
PBC	porcine sequence →				
PKS	porcine sequence →				
Baboon	KEVATSVQLT	LSSKKDYLHG	DNSDIIPTDT	IKNTVHVLAK	80
Porcine	FKGIKSIETF	AVTICEHFLS	SFKHVIRAQV	YVEEVPWKRF	120
PBC	porcine sequence →				
PKS	porcine sequence →				
Baboon	FKGIKSIEAF	GVNICEYFLS	SFNHVIRAQV	YVEEIPWKRL	120
Porcine	EKNGVKHVHA	FIYTPTGTHF	CEVEQIRNGP	PVIHSGIKDL	160
PBC	porcine sequence →				
PKS	porcine sequence →				
Baboon	EKNGVKHVHA	FIHTPTGTHF	CEVEQLRSGP	PVIHSGIKDL	160
Porcine	KVLKTTQSGF	EGFIKDQFTT	LPEVKDRCFA	TQVYCKWRYH	200
PBC	porcine sequence →				
PKS	porcine sequence →				
Baboon	KVLKTTQSGF	EGFIKDQFTT	LPEVKDRCFA	TQVYCKWRYH	200
Porcine	QGRDVDPEAT	WDTVRSIVLQ	KFAGPYDKGE	YSPSVQKTLY	240
PBC	porcine sequence → ← baboon sequence				
PKS	porcine sequence →				
Baboon	QCRDVDPEAT	WGTIRDLVLE	KFAGPYDKGE	YSPSVQKTLY	240
Porcine	DIQVLTGQV	PEIEDMEISL	PNIHYLNIDM	SKMGLINKEE	280
PBC	baboon sequence →				
PKS	porcine sequence →				
Baboon	DIQVLSLSRV	PEIEDMEISL	PNIHYFNIDM	SKMGLINKEE	280
Porcine	VLLPLDNPYG	RITGTVKRKL	TSRL		
PBC	baboon sequence →				304
PKS	porcine ← baboon 289-304				
Baboon	VLLPLDNPYG	KITGTVKRKL	SSRL		

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Fig. 6

Comparison of amino acid sequences "stripped-down" version of chimera, known as "PigKS" (also called "Pig-Lys") vs. Pig uricase

"Pig KS" uricase:

Pig cDNA from 1 to 864 (NdeI site) and then Baboon 865 to 915 (end)

Pig uricase:

Pig cDNA from 1 to 915 (end)

[GCG GAP program]

Gap Weight: 12 Average Match: 2.912
Length Weight: 4 Average Mismatch: -2.003

Quality: 1601 Length: 319
Ratio: 5.249 Gaps: 0
Percent Similarity: 99.672 Percent Identity: 99.344

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

pigKS.pep x Pig.pep June 25, 1998 17:11 ..

```

pigKS  1 MAHYRNDYKKNDEVEFVRTGYGKDMIKVLHIQRDGKYHSIKEVATSVQLT  50
      |||
Pig    1 MAHYRNDYKKNDEVEFVRTGYGKDMIKVLHIQRDGKYHSIKEVATSVQLT  50

      51 LSSKKDYLHGDNSDVIPTDTIKNTVNVLAKFKGIKSIETFAVTICEHFLS  100
      |||
      51 LSSKKDYLHGDNSDVIPTDTIKNTVNVLAKFKGIKSIETFAVTICEHFLS  100

     101 SFKHVIRAQVYVEEVPWKRFEKNGVKHVHAFIYTPTGTHFCEVEQIRNGP  150
      |||
     101 SFKHVIRAQVYVEEVPWKRFEKNGVKHVHAFIYTPTGTHFCEVEQIRNGP  150

     151 PVIHSGIKDLKVLKTTQSGFEGFIKDQFTTLPEVKDRCFATQVYCKWRYH  200
      |||
     151 PVIHSGIKDLKVLKTTQSGFEGFIKDQFTTLPEVKDRCFATQVYCKWRYH  200

     201 QGRDVFDFEATWDTVRSIVLQKFAGPYDKGEYSPSVQKTLYDIQVLTGLQV  250
      |||
     201 QGRDVFDFEATWDTVRSIVLQKFAGPYDKGEYSPSVQKTLYDIQVLTGLQV  250

     251 PEIEDMEISLPNIHYLNIDMSKMGLINKKEEVLLPLDNPYGRITGTVKRKL  300
      |||
     251 PEIEDMEISLPNIHYLNIDMSKMGLINKKEEVLLPLDNPYGRITGTVKRKL  300

     301 SSRL*   305
      .|||
     301 TSRL*   305
  
```

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Fig. 7

Comparison of amino acid sequences of the "original" Pig-baboon chimeric uricase ("chimera") with that of the "stripped-down" version of chimera, known as "PigKS" (also called "Pig-Lys")

"Chimera" uricase:

Pig cDNA from 1 to 674 (Apa site) and then Baboon cDNA from 675 to 915 (end)

"Pig KS" uricase:

Pig cDNA from 1 to 864 (NdeI site) and then Baboon 865 to 915 (end)

{GCG GAP program}

Gap Weight:	12	Average Match:	2.912
Length Weight:	4	Average Mismatch:	-2.003
Quality:	1589	Length:	319
Ratio:	5.210	Gaps:	0
Percent Similarity:	98.689	Percent Identity:	98.689

Match display thresholds for the alignment(s):

```

      | = IDENTITY
      : = 2
      . = 1
  
```

chimera.pep x pigKS.pep June 25, 1998 16:15 ..

```

chim.  1 MAHYRNDYKKNDEVEFVRTGYGKDMIKVLHIQRDGKYHSIKEVATSVQLT 50
      |||||||||||||||||||||||||||||||||||||||||||||||||||
PigKS  1 MAHYRNDYKKNDEVEFVRTGYGKDMIKVLHIQRDGKYHSIKEVATSVQLT 50
      |||||||||||||||||||||||||||||||||||||||||||||||||||

      51 LSSKKDYLHGDNSDVIPTDTIKNTVNVLAKFKGIKSIETFAVTICEHFLS 100
      |||||||||||||||||||||||||||||||||||||||||||||||||||
      51 LSSKKDYLHGDNSDVIPTDTIKNTVNVLAKFKGIKSIETFAVTICEHFLS 100
      |||||||||||||||||||||||||||||||||||||||||||||||||||

     101 SFKHVIRAQVYVEEVPWKRFEKNGVKHVHAFIYTPGTGTHFCEVEQIRNGP 150
      |||||||||||||||||||||||||||||||||||||||||||||||||||
     101 SFKHVIRAQVYVEEVPWKRFEKNGVKHVHAFIYTPGTGTHFCEVEQIRNGP 150
      |||||||||||||||||||||||||||||||||||||||||||||||||||

     151 PVIHSGIKDLKVLKTTQSGFEGFIKDQFTTLPEVKDRCFATQVYCKWRYH 200
      |||||||||||||||||||||||||||||||||||||||||||||||||||
     151 PVIHSGIKDLKVLKTTQSGFEGFIKDQFTTLPEVKDRCFATQVYCKWRYH 200
      |||||||||||||||||||||||||||||||||||||||||||||||||||

     201 QGRDVFDEATWDTVRSIVLQKFAGPYDKGEYSPSVQKTLYDIQVLSLSRV 250
      |||||||||||||||||||||||||||||||||||||||||||||||||||
     201 QGRDVFDEATWDTVRSIVLQKFAGPYDKGEYSPSVQKTLYDIQVLTGQV 250
      |||||||||||||||||||||||||||||||||||||||||||||||||||

     251 PEIEDMEISLPNIHYFNIDMSKMGLINKEEVLLPLDNPYGKITGTVKRKL 300
      |||||||||||||||||||||||||||||||||||||||||||||||||||
     251 PEIEDMEISLPNIHYLNIDMSKMGLINKEEVLLPLDNPYGKITGTVKRKL 300
      |||||||||||||||||||||||||||||||||||||||||||||||||||

     301 SSRL* 305
      |||||
     301 SSRL* 305
  
```

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Fig. 8

Comparison of amino acid sequences of the "original" Pig-baboon chimeric uricase ("chimera") with that of Pig uricase

"Chimera" uricase:

Pig cDNA from 1 to 674 (Apa site) and then Baboon cDNA from 675 to 915 (end)

Pig uricase:

Pig cDNA from 1 to 915 (end)

[GCG GAP program]

Gap Weight: 12 Average Match: 2.912
Length Weight: 4 Average Mismatch: -2.003

Quality: 1583 Length: 305
Ratio: 5.190 Gaps: 0
Percent Similarity: 98.361 Percent Identity: 98.033

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

chimera.pep x Pig.pep June 25, 1998 16:54 ..

```

chim  1 MAHYRNDYKKNDEVEFVRTGYGKDMIKVLHIQRDGGKYHSIKEVATSVQLT  50
      |||
Pig   1 MAHYRNDYKKNDEVEFVRTGYGKDMIKVLHIQRDGGKYHSIKEVATSVQLT  50
      |||

51  LSSKKDYLHGDNSDVIPTDTIKNTVNVLAKEFKGIKSIETFAVTICEHFLS  100
      |||
51  LSSKKDYLHGDNSDVIPTDTIKNTVNVLAKEFKGIKSIETFAVTICEHFLS  100
      |||

101  SFKHVIRAQVYVEEVPWKRFEKNGVKHVHAFIYTPTGTHFCEVEQIRNGP  150
      |||
101  SFKHVIRAQVYVEEVPWKRFEKNGVKHVHAFIYTPTGTHFCEVEQIRNGP  150
      |||

151  PVIHSGIKDLKVLKTTQSGFEGFIKDQFTTLPEVKDRCFATQVYCKWRYH  200
      |||
151  PVIHSGIKDLKVLKTTQSGFEGFIKDQFTTLPEVKDRCFATQVYCKWRYH  200
      |||

201  QGRDVFDEATWDTVRSIVLQKFAGPYDKGEYSPSVQKTLYDIQVLSLSRV  250
      |||
201  QGRDVFDEATWDTVRSIVLQKFAGPYDKGEYSPSVQKTLYDIQVLTGQV  250
      |||

251  PEIEDMEISLPNIHYFNIDMSKMGLINKEEVLLPLDNPYGKITGTVKRKL  300
      |||
251  PEIEDMEISLPNIHYLNIDMSKMGLINKEEVLLPLDNPYGRITGTVKRKL  300
      |||

301  SSRL* 305
      .|||
301  TSRL* 305

```


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Fig. 9

Comparison of amino acid sequence of the "original" Pig-baboon chimeric uricase ("chimera") with that of "Baboon D3H" uricase (Baboon except for His replacing Asp at amino acid 3)

Pig uricase:

Pig cDNA from 1 to 915 (end)

"Baboon D3H" uricase:

"Baboon D3H" cDNA from 1 to 915 (end)

[GCG GAP program]

Gap Weight: 12 Average Match: 2.912
Length Weight: 4 Average Mismatch: -2.003

Quality: 1493 Length: 305
Ratio: 4.895 Gaps: 0
Percent Similarity: 94.098 Percent Identity: 90.820

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

Pig.pep x baboon D3H.pep

June 25, 1998 17:44 ..

```

Pig  1 MAHYRNDYKKNDEVEFVRTGYGKDMIKVLHIQRDGKYHSIKEVATSVQLT  50
      |||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.
Bab  1 MAHYNNYKKNDELEFVRTGYGKDMVKVLHIQRDGKYHSIKEVATSVQLT  50
      |||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.
      51 LSSKKDYLGHDNSDVIPTDTIKNTVNVLAKFKGIKSIETFAVTICEHFLS  100
      |||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.
      51 LSSKKDYLGHDNSDIIPTDTIKNTVHVLAKEFKGIKSIEAFGVNICEYFLS  100
      |||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.
      101 SFKHVIRAQVYVEEVPWKRFEKNGVKHVHAFIYTPGTGTHFCEVEQIRNGP  150
      |||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.
      101 SFNHVIRAQVYVEEIPWKRLEKNGVKHVHAFIHTPTGTHFCEVEQLRSGP  150
      |||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.
      151 PVIHSGIKDLKVLKTTQSGFEGFIKDQFTTLPEVKDRCFATQVYCKWRYH  200
      |||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.
      151 PVIHSGIKDLKVLKTTQSGFEGFIKDQFTTLPEVKDRCFATQVYCKWRYH  200
      |||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.
      201 QGRDVFDEATWDTVRSIVLQKFAGPYDKGEYSPSVQKTLYDIQVLTGLGQV  250
      |||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.
      201 QCRDVFDEATWGTIRDLVLEKFAGPYDKGEYSPSVQKTLYDIQVLSLSRV  250
      |||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.
      251 PEIEDMEISLPNIHYLNIDMSKMGLINKEEVLLPLDNPYGRITGTVKKRL  300
      |||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.
      251 PEIEDMEISLPNIHYFNIDMSKMGLINKEEVLLPLDNPYGKITGTVKKRL  300
      |||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.
      301 TSRL* 305
      .|||||
      301 SSRL* 305
  
```

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Fig. 10

Comparison of amino acid sequence of the "original" Pig-baboon chimeric uricase ("chimera") with that of "Baboon D3H" uricase (Baboon except for His replacing Asp at amino acid 3)

"Chimera" uricase:

Pig cDNA from 1 to 674 (Apa site) and then Baboon cDNA from 675 to 915 (end)

"Baboon D3H" uricase:

"Baboon D3H" cDNA from 1 to 915 (end)

[GCG GAP program]

Gap Weight:	12	Average Match:	2.912
Length Weight:	4	Average Mismatch:	-2.003
Quality:	1516	Length:	305
Ratio:	4.970	Gaps:	0
Percent Similarity:	95.738	Percent Identity:	92.787

Match display thresholds for the alignment(s):

```

| = IDENTITY
: = 2
. = 1

```

chimera.pep x baboon D3H.pep June 25, 1998 17:18 ..

```

chim  1 MAHYRNDYKKNDEVEFVRTGYGKDMIKVLHIQRDGKYHSIKEVATSVQLT  50
      ||||| |.|||||.|||||:|||||
Bab   1 MAHYHNNYKKNDELEFVRTGYGKDMVKVLHIQRDGKYHSIKEVATSVQLT  50
      ||||| |.|||||.|||||:|||||

51  LSSKKDYLHGDNSDVIPTDTIKNTVMVLAKFKGIKSIETFAVTICEHFLS  100
      ||||| |.|||||.|||||:|||||
51  LSSKKDYLHGDNSDIIPTDTIKNTVHVLAKFKGIKSIIEAFGVNICEYFLS  100
      ||||| |.|||||.|||||:|||||

101 SFKHVIRAQVYVEEVPWKRFEKNGVKHVHAFIYPTPTGTHFCEVEQIRNGP  150
      ||||| |.|||||.|||||:|||||
101 SFNHVIRAQVYVEEIPWKRLEKNGVKHVHAFIHTPTGTHFCEVEQLRSGP  150
      ||||| |.|||||.|||||:|||||

151 PVIHSGIKDLKVLKTTQSGFEGFIKDQFTTLPEVKDRCFATQVYCKWRYH  200
      ||||| |.|||||.|||||:|||||
151 PVIHSGIKDLKVLKTTQSGFEGFIKDQFTTLPEVKDRCFATQVYCKWRYH  200
      ||||| |.|||||.|||||:|||||

201 QGRDVFDEATWDTVRSIVLQKFAGPYDKGEYSPSVQKTLYDIQVLSLSRV  250
      ||||| |.|||||.|||||:|||||
201 QCRDVFDEATWGTIRDLVLEKAGPYDKGEYSPSVQKTLYDIQVLSLSRV  250
      ||||| |.|||||.|||||:|||||

251 PEIEDMEISLPNIHYFNIDMSKMGLINKEEVLLPLDNPYGKITGTGTVKRKL  300
      ||||| |.|||||.|||||:|||||
251 PEIEDMEISLPNIHYFNIDMSKMGLINKEEVLLPLDNPYGKITGTGTVKRKL  300
      ||||| |.|||||.|||||:|||||

301 SSRL* 305
      |||||
301 SSRL* 305

```

11/18

Fig. 11-1

Bestfit (GCG software) comparison of coding sequences of the cDNAs of Pig KS uricase ("PKS") vs. pig uricase

"Pig KS" uricase:

Pig cDNA from 1 to 864 (NdeI site) and then Baboon 865 to 915 (end)

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	-9.000

Quality:	9036	Length:	915
Ratio:	9.875	Gaps:	0
Percent Similarity:	99.344	Percent Identity:	99.344

Match display thresholds for the alignment(s):

	=	IDENTITY
:	=	5
.	=	1

pigKS.seq x pig.seq July 25, 1998 10:14 ..

```

PKS   1 ATGGCTCATTACCGTAATGACTACAAAAAGAATGATGAGGTAGAGTTTGT 50
      |||||||
pig   1 ATGGCTCATTACCGTAATGACTACAAAAAGAATGATGAGGTAGAGTTTGT 50
      |||||||

      51 CCGAACTGGCTATGGGAAGGATATGATAAAAGTTCTCCATATTCAGCGAG 100
      |||||||
      51 CCGAACTGGCTATGGGAAGGATATGATAAAAGTTCTCCATATTCAGCGAG 100
      |||||||

     101 ATGGAAAATATCACAGCATTAAGAGGTGGCAACTTCAGTGCAACTGACT 150
      |||||||
     101 ATGGAAAATATCACAGCATTAAGAGGTGGCAACTTCAGTGCAACTGACT 150
      |||||||

     151 TTGAGCTCCAAAAAGATTACCTGCATGGAGACAATTCAGATGTCATCCC 200
      |||||||
     151 TTGAGCTCCAAAAAGATTACCTGCATGGAGACAATTCAGATGTCATCCC 200
      |||||||

     201 TACAGACACCATCAAGAACACAGTTAATGTCCTGGCGAAGTTCAAAGGCA 250
      |||||||
     201 TACAGACACCATCAAGAACACAGTTAATGTCCTGGCGAAGTTCAAAGGCA 250
      |||||||

     251 TCAAAAGCATAGAACTTTTGCTGTGACTATCTGTGAGCATTTCCTTTCT 300
      |||||||
     251 TCAAAAGCATAGAACTTTTGCTGTGACTATCTGTGAGCATTTCCTTTCT 300
      |||||||

     301 TCCTTCAAGCATGTCATCAGAGCTCAAGTCTATGTGGAAGAAGTTCCTTG 350
      |||||||
     301 TCCTTCAAGCATGTCATCAGAGCTCAAGTCTATGTGGAAGAAGTTCCTTG 350
      |||||||

     351 GAAGCGTTTTTGAAAAGAATGGAGTTAAGCATGTCCATGCATTTATTATA 400
      |||||||
     351 GAAGCGTTTTTGAAAAGAATGGAGTTAAGCATGTCCATGCATTTATTATA 400
      |||||||
  
```

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Fig. 11-2

401 CTCCTACTGGAACGCACTTCTGTGAGGTTGAACAGATAAGGAATGGACCT 450
|||
401 CTCCTACTGGAACGCACTTCTGTGAGGTTGAACAGATAAGGAATGGACCT 450
451 CCAGTCATTTCATTCTGGAATCAAAGACCTAAAAGTCTTGAAAACAACCCA 500
|||
451 CCAGTCATTTCATTCTGGAATCAAAGACCTAAAAGTCTTGAAAACAACCCA 500
501 GTCTGGCTTTGAAGGATTCATCAAGGACCAGTTCACCACCCTCCCTGAGG 550
|||
501 GTCTGGCTTTGAAGGATTCATCAAGGACCAGTTCACCACCCTCCCTGAGG 550
551 TGAAGGACCGGTGCTTTGCCACCCAAGTGTACTGCAAATGGCGCTACCAC 600
|||
551 TGAAGGACCGGTGCTTTGCCACCCAAGTGTACTGCAAATGGCGCTACCAC 600
601 CAGGGCAGAGATGTGGACTTTGAGGCCACCTGGGACACTGTTAGGAGCAT 650
|||
601 CAGGGCAGAGATGTGGACTTTGAGGCCACCTGGGACACTGTTAGGAGCAT 650
651 TGTCTGCAGAAATTTGCTGGGCCCTATGACAAAGGCGAGTACTCGCCCT 700
|||
651 TGTCTGCAGAAATTTGCTGGGCCCTATGACAAAGGCGAGTACTCGCCCT 700
701 CTGTCCAGAAGACACTCTATGACATCCAGGTGCTCACCTGGGCCAGGTT 750
|||
701 CTGTCCAGAAGACACTCTATGACATCCAGGTGCTCACCTGGGCCAGGTT 750
751 CCTGAGATAGAAGATATGGAAATCAGCCTGCCAAATATTCACTACTTAAA 800
|||
751 CCTGAGATAGAAGATATGGAAATCAGCCTGCCAAATATTCACTACTTAAA 800
801 CATAGACATGTCCAAATGGGACTGATCAACAAGGAAGAGGTCTTGCTAC 850
|||
801 CATAGACATGTCCAAATGGGACTGATCAACAAGGAAGAGGTCTTGCTAC 850
851 CTTTAGACAATCCATATGGAAAAATTACTGGTACAGTCAAGAGGAAGTTG 900
|||
851 CTTTAGACAATCCATATGGCAGGATTACTGGTACAGTCAAGAGGAAGCTG 900
901 TCTTCAAGACTGTGA 915
|||
901 ACTTCAAGGCTGTGA 915

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Fig. 12-1

Bestfit (GCG software) comparison of coding sequences of the cDNAs of Pig KS uricase ("PKS") vs. baboon uricase

"Pig KS" uricase:

Pig cDNA from 1 to 864 (NdeI site) and then Baboon 865 to 915 (end)

Gap Weight: 50 Average Match: 10.000
Length Weight: 3 Average Mismatch: -9.000

Quality: 7573 Length: 915
Ratio: 8.277 Gaps: 0
Percent Similarity: 90.929 Percent Identity: 90.929

Match display thresholds for the alignment(s):

| = IDENTITY
: = 5
. = 1

pigKS.seq x baboon.seq July 25, 1998 10:21 ..

```

PKS   1 ATGGCTCATTACCGTAATGACTACAAAAGAATGATGAGGTAGAGTTTGT  50
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
bab   1 ATGGCCGACTACCATAACAACATAAAAAGAATGATGAATTGGAGTTTGT  50
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

      51 CCGAACTGGCTATGGGAAGGATATGATAAAAGTTCTCCATATTCAGCGAG 100
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
      51 CCGAACTGGCTATGGGAAGGATATGGTAAAAGTTCTCCATATTCAGCGAG 100
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

     101 ATGGAAAATATCACAGCATTAAAGAGGTGGCAACTTCAGTGCAACTGACT 150
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
     101 ATGGAAAATATCACAGCATTAAAGAGGTGGCAACTTCAGTGCAACTTACT 150
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

     151 TTGAGCTCCAAAAAGATTACCTGCATGGAGACAATTCAGATGTCATCCC 200
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
     151 CTGAGTTCCAAAAAGATTACCTGCATGGAGATAATTCAGATATCATCCC 200
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

     201 TACAGACACCATCAAGAACACAGTTAATGTCCTGGCGAAGTTCAAAGGCA 250
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
     201 TACAGACACCATCAAGAACACAGTTCATGTCTTGGCAAAGTTTAAGGGAA 250
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

     251 TCAAAGCATAGAACTTTTGCTGTGACTATCTGTGAGCATTTCCTTTCT 300
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
     251 TCAAAGCATAGAAAGCCTTTGGTGTGAATATTTGTGAGTATTTTCTTTCT 300
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

     301 TCCTTCAAGCATGTTCATCAGAGCTCAAGTCTATGTGGAAGAAGTTCCCTTG 350
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
     301 TCTTTTAACCATGTAATCCGAGCTCAAGTCTACGTGGAAGAAATCCCTTG 350
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

     351 GAAGCGTTTTGAAAAGAATGGAGTTAAGCATGTCCATGCATTTATTATATA 400
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
     351 GAAGCGTCTTGAAAAGAATGGAGTTAAGCATGTCCATGCATTTATTACACA 400
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
  
```

[illegible]

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Fig. 13-1

Bestfit (GCG software) comparison of coding sequences of the cDNAs of "original" pig-baboon chimeric uricase ("PBC") vs. pig uricase

"PBC" uricase:

Pig cDNA from 1 to 674 (Apa site) then Baboon cDNA from 675 to 915 (end). PBC chimeric cDNA can be cut out with NcoI plus BamHI

Gap Weight: 50 Average Match: 10.000
Length Weight: 3 Average Mismatch: -9.000

Quality: 8770 Length: 915
Ratio: 9.585 Gaps: 0
Percent Similarity: 97.814 Percent Identity: 97.814

Match display thresholds for the alignment(s):

| = IDENTITY
: = 5
. = 1

PBC.seq x pig.seq

July 25, 1998 08:10 ..

```

PBC   1 ATGGCTCATTACCGTAATGACTACAAAAAGAATGATGAGGTAGAGTTTGT 50
      |||
PIG   1 ATGGCTCATTACCGTAATGACTACAAAAAGAATGATGAGGTAGAGTTTGT 50
      |||

51  CCGAACTGGCTATGGGAAGGATATGATAAAAGTTCTCCATATTCAGCGAG 100
      |||
51  CCGAACTGGCTATGGGAAGGATATGATAAAAGTTCTCCATATTCAGCGAG 100
      |||

101 ATGGAAAATATCACAGCATTAAAGAGGTGGCAACTTCAGTGCAACTGACT 150
      |||
101 ATGGAAAATATCACAGCATTAAAGAGGTGGCAACTTCAGTGCAACTGACT 150
      |||

151 TTGAGCTCCAAAAAGATTACCTGCATGGAGACAATTCAGATGTCATCCC 200
      |||
151 TTGAGCTCCAAAAAGATTACCTGCATGGAGACAATTCAGATGTCATCCC 200
      |||

201 TACAGACACCATCAAGAACACAGTTAATGTCCTGGCGAAGTTCAAAGGCA 250
      |||
201 TACAGACACCATCAAGAACACAGTTAATGTCCTGGCGAAGTTCAAAGGCA 250
      |||

251 TCAAAAGCATAGAACTTTTGCTGTGACTATCTGTGAGCATTTCCTTTCT 300
      |||
251 TCAAAAGCATAGAACTTTTGCTGTGACTATCTGTGAGCATTTCCTTTCT 300
      |||

301 TCCTTCAAGCATGTCATCAGAGCTCAAGTCTATGTGGAAGAAGTTCCTTG 350
      |||
301 TCCTTCAAGCATGTCATCAGAGCTCAAGTCTATGTGGAAGAAGTTCCTTG 350
      |||

351 GAAGCGTTTGGAAAAGAATGGAGTTAAGCATGTCCATGCATTTATTATTA 400
      |||
351 GAAGCGTTTGGAAAAGAATGGAGTTAAGCATGTCCATGCATTTATTATTA 400
      |||

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Fig. 13-2

401 CTCCTACTGGAACGCACTTCTGTGAGGTTGAACAGATAAGGAATGGACCT 450
|||||
401 CTCCTACTGGAACGCACTTCTGTGAGGTTGAACAGATAAGGAATGGACCT 450
451 CCAGTCATTCATTCTGGAATCAAAGACCTAAAAGTCTTGAAAACAACCCA 500
|||||
451 CCAGTCATTCATTCTGGAATCAAAGACCTAAAAGTCTTGAAAACAACCCA 500
501 GTCTGGCTTTGAAGGATTCATCAAGGACCAGTTCACCACCCTCCCTGAGG 550
|||||
501 GTCTGGCTTTGAAGGATTCATCAAGGACCAGTTCACCACCCTCCCTGAGG 550
551 TGAAGGACCGGTGCTTTGCCACCCAAGTGTAAGTGCATGCGCTACCAC 600
|||||
551 TGAAGGACCGGTGCTTTGCCACCCAAGTGTAAGTGCATGCGCTACCAC 600
601 CAGGGCAGAGATGTGGACTTTGAGGCCACCTGGGACACTGTTAGGAGCAT 650
|||||
601 CAGGGCAGAGATGTGGACTTTGAGGCCACCTGGGACACTGTTAGGAGCAT 650
651 TGTCCCTGCAGAAATTTGCTGGGCCCTATGACAAAGGCGAGTACTCACCT 700
|||||
651 TGTCCCTGCAGAAATTTGCTGGGCCCTATGACAAAGGCGAGTACTCGCCCT 700
701 CTGTGCAGAAAGACCCTCTATGATATCCAGGTGCTCTCCCTGAGCCGAGTT 750
|||||
701 CTGTCCAGAAAGACACTCTATGACATCCAGGTGCTCACCTGGGCCAGGTT 750
751 CCTGAGATAGAAGATATGGAAATCAGCCTGCCAAACATTCACACTTCAA 800
|||||
751 CCTGAGATAGAAGATATGGAAATCAGCCTGCCAAATATTCACACTTAAA 800
801 TATAGACATGTCCAAAATGGGTCTGATCAACAAGGAAGAGGTCTTGCTGC 850
|||||
801 CATAGACATGTCCAAAATGGGACTGATCAACAAGGAAGAGGTCTTGCTAC 850
851 CATTAGACAATCCATATGGAAAAATTACTGGTACAGTCAAGAGGAAGTTG 900
|||||
851 CTTTAGACAATCCATATGGCAGGATTACTGGTACAGTCAAGAGGAAGCTG 900
901 TCTTCAAGACTGTGA 915
|||||
901 ACTTCAAGGCTGTGA 915

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Fig. 14-1

Bestfit (GCG software) comparison of coding sequences of the cDNAs of "original" pig-baboon chimeric uricase ("PBC") vs. baboon uricase

"PBC" uricase:

Pig cDNA from 1 to 674 (Apa site) then Baboon cDNA from 675 to 915 (end). PBC chimeric cDNA can be cut out with NcoI plus BamHI

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	-9.000
Quality:	7839	Length:	915
Ratio:	8.567	Gaps:	0
Percent Similarity:	92.459	Percent Identity:	92.459

Match display thresholds for the alignment(s):

```

| = IDENTITY
: = 5
. = 1

```

PBC.seq x Wubaboon.seq July 25, 1998 09:36 ..

```

PBC   1 ATGGCTCATTACCGTAATGACTACAAAAAGAATGATGAGGTAGAGTTTGT 50
      ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Bab   1 ATGGCCGACTACCATAACAACATAAAAAAGAATGATGAATTGGAGTTTGT 50
      ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      51 CCGAACTGGCTATGGGAAGGATATGATAAAAGTTCTCCATATTCAGCGAG 100
      ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      51 CCGAACTGGCTATGGGAAGGATATGGTAAAAGTTCTCCATATTCAGCGAG 100
      ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      101 ATGGAAAATATCACAGCATTAAGAGGTGGCAACTTCAGTGCAACTGACT 150
      ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      101 ATGGAAAATATCACAGCATTAAGAGGTGGCAACTTCAGTGCAACTTACT 150
      ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      151 TTGAGCTCCAAAAAGATTACCTGCATGGAGACAATTCAGATGTCATCCC 200
      ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      151 CTGAGTTCCAAAAAGATTACCTGCATGGAGATAATTCAGATATCATCCC 200
      ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      201 TACAGACACCATCAAGAACACAGTTAATGTCCTGGCGAAGTTCAAAGGCA 250
      ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      201 TACAGACACCATCAAGAACACAGTTCATGTCTTGCAAAGTTTAAGGGAA 250
      ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      251 TCAAAAGCATAGAACTTTTGCTGTGACTATCTGTGAGCATTTTCTTTCT 300
      ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      251 TCAAAAGCATAGAAAGCCTTTGGTGTGAATATTTGTGAGTATTTTCTTTCT 300
      ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      301 TCCTTCAAGCATGTCATCAGAGCTCAAGTCTATGTGGAAGAAGTTCCTTG 350
      ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      301 TCTTTTAACCATGTAATCCGAGCTCAAGTCTACGTGGAAGAAATCCCTTG 350
      ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      351 GAAGCGTTTTTGAAAAGAATGGAGTTAAGCATGTCCATGCATTTATTTATA 400
      ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      351 GAAGCGTCTTGAAAAGAATGGAGTTAAGCATGTCCATGCATTTATTCACA 400
      ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Fig. 14-2

401 CTCCTACTGGAACGCACCTTCTGTGAGGTTGAACAGATAAGGAATGGACCT 450
|||||
401 CTCCCACTGGAACACACTTCTGTGAAGTTGAACAACCTGAGAAGTGGACCC 450
451 CCAGTCATTTCATTCTGGAATCAAAGACCTAAAAGTCTTGAAAACAACCCA 500
|||
451 CCCGTCATTTCATTCTGGAATCAAAGACCTCAAGGTCTTGAAAACAACACA 500
501 GTCTGGCTTTGAAGGATTCATCAAGGACCAGTTCACCACCCTCCCTGAGG 550
|||||
501 GTCTGGATTTGAAGGTTTCATCAAGGACCAGTTCACCACCCTCCCTGAGG 550
551 TGAAGGACCGGTGCTTTGCCACCCAAGTGTAAGTGCAGTGGCGCTACCAC 600
|||||
551 TGAAGGACCGATGCTTTGCCACCCAAGTGTAAGTGCAGTGGCGCTACCAC 600
601 CAGGGCAGAGATGTGGACTTTGAGGCCACCTGGGACACTGTTAGGAGCAT 650
|||
601 CAGTGCAGGGATGTGGACTTCGAGGCTACCTGGGGCACCATTCTGGGACCT 650
651 TGTCTGCAGAAATTTGCTGGGCCCTATGACAAAGGCGAGTACTCACCT 700
|||||
651 TGTCTGGAGAAATTTGCTGGGCCCTATGACAAAGGCGAGTACTCACCT 700
701 CTGTGCAGAAGACCCTCTATGATATCCAGGTGCTCTCCCTGAGCCGAGTT 750
|||||
701 CTGTGCAGAAGACCCTCTATGATATCCAGGTGCTCTCCCTGAGCCGAGTT 750
751 CCTGAGATAGAAGATATGGAAATCAGCCTGCCAAACATTCACACTTTCAA 800
|||||
751 CCTGAGATAGAAGATATGGAAATCAGCCTGCCAAACATTCACACTTTCAA 800
801 TATAGACATGTCCAAAATGGGTCTGATCAACAAGGAAGAGGTCTTGCTGC 850
|||||
801 TATAGACATGTCCAAAATGGGTCTGATCAACAAGGAAGAGGTCTTGCTGC 850
851 CATTAGACAATCCATATGGAAAAATTACTGGTACAGTCAAGAGGAAGTTG 900
|||||
851 CATTAGACAATCCATATGGAAAAATTACTGGTACAGTCAAGAGGAAGTTG 900
901 TCTTCAAGACTGTGA 915
|||||
901 TCTTCAAGACTGTGA 915